

**SEQUENCE LISTING**

1103 Salom et al.

<120> DNA Encoding A Human Melanin Concentrating Hormone Receptor (MCH1) And Uses Thereof

<130> 1795/57453=C/JPW

<140> NotYetKnown

<141> 2001-07-05

<150> 09/610,635

<151> 2000-07-05

<160> 28

<170> PatentIn Ver. 2.1

<210> 1

<211> 1269

<212> DNA

<210> 2  
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 <213> Homo sapiens

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Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro 35                   40                   45
Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala 50                   55                   60
Thr Gly Thr Gly Trp Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly 65                   70                   75                   80
Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala 85                   90                   95
Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met 100                105                110
Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser 115                120                125
Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn 130                135                140
Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu 145                150                155                160
Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly 165                170                175
Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp 180                185                190
Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile 195                200                205
Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg 210                215                220

T050700-22266860

PDSUQCD3C269890

Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser  
 225 230 235 240

Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe  
 245 250 255

Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr  
 260 265 270

Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu  
 275 280 285

Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met  
 290 295 300

Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr  
 305 310 315 320

Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val  
 325 330 335

Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser  
 340 345 350

Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu  
 355 360 365

Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys  
 370 375 380

Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln  
 385 390 395 400

Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg  
 405 410 415

Thr Glu Ser Lys Gly Thr  
 420

<210> 3  
<211> 1214  
<212> DNA  
<213> Rattus norvegicus

<400> 3  
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<210> 4  
<211> 353  
<212> PRT  
<213> *Rattus norvegicus*

<400> 4

Met Asp Leu Gln Thr Ser Leu Leu Ser Thr Gly Pro Asn Ala Ser Asn  
1 5 10 15

Ile Ser Asp Gly Gln Asp Asn Leu Thr Leu Pro Gly Ser Pro Pro Arg  
30 35 30

Thr Gly Ser Val Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly  
35 40 45

Thr Ile Cys Leu Leu Gly Ile Val Gly Asn Ser Thr Val Ile Phe Ala  
50 55 60

Val Val Lys Lys Ser Lys Leu His Trp Cys Ser Asn Val Pro Asp Ile  
15 50 75 80

Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met  
55 60 65

Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly

EUSQD \* 26466360

Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe			
115	120	125	
Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala			
130	135	140	
Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Met Ala			
145	150	155	160
Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr			
165	170	175	
Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val			
180	185	190	
Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe			
195	200	205	
Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile			
210	215	220	
Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala			
225	230	235	240
Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg			
245	250	255	
Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr			
260	265	270	
Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr			
275	280	285	
Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser			
290	295	300	
Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys			
305	310	315	320
Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Thr			
325	330	335	
Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly			
340	345	350	

Thr

2025020 = 222063650

<210> 5  
<211> 26  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer/probe  
  
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gggaactcca cggtcatctt cgccgt

26

<210> 6  
<211> 26  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer/probe  
  
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tagcggtcaa tggccatggc ggtcag

26

<210> 7  
<211> 45  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer/probe  
  
<400> 7  
ctcctggca tgcccttcat gatccaccag ctcatggca atggg

45

<210> 8  
<211> 25  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer/probe  
  
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cttcttaggc tgtacggaag tgtta

25

<210> 9  
<211> 27  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 9  
gttgtggttt gtccaaactc atcaatg 27

<210> 10  
<211> 37  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 10  
cgcggatcca ttatgtctgc actccgaagg aaatttg 37

<210> 11  
<211> 38  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 11  
cgcgaattct tatgtgaagc gatcagagtt cattttc 38

<210> 12  
<211> 34  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 12  
gcgggatccg ctagggctgg tgattctagg aatg 34

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<210> 13
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

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ccggaattcc cctcacacccg agccccctgg

<210> 14
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 14
tcagctcggt tgtgggagca

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<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<400> 15
cttggacttc ttcacgac

<210> 16
<211> 100
<212> PRT
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<220>
<223> Description of Artificial Sequence: mutated human
      MCH1

<400> 16
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PDB ID: 2C246960

Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Thr Ala Val Gly Leu  
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Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp  
20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Arg Arg Trp Arg Leu Pro  
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala  
50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly  
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala  
85 90 95

Gly Ser Pro Pro  
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<210> 17

<211> 100

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mutated human  
MCH1

<400> 17

Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu  
1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp  
20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Arg Arg Trp Arg Leu Pro  
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala  
50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly  
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala

105020 3E266860

85

90

95

Gly Ser Pro Pro  
100

<210> 18  
<211> 31  
<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer/probe

<400> 18

cggcactggc tggcgccacc tggaaggctc g

31

<210> 19  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 19

cgaggcgttc aggtccgcacc agccagtgcc g

31

<210> 20  
<211> 32  
<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer/probe

<400> 20

atgtcagtgg gagccgcgaa gaagggagtg gg

32

<210> 21  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>

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TUSC2000-202469360

<223> Description of Artificial Sequence: primer/probe

<400> 21

cccaactccct ttttcgcggc tcccactgac at

32

<210> 22

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer/probe

<400> 22

taatgtgtct aggtggcgctc agtgggagcc atg

33

<210> 23

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer/probe

<400> 23

catggctccc actgacgcca cctagacaca tta

33

<210> 24

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 24

tgacactaaag cttcactggc tggatggacc tggaagg

37

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer/probe

<400> 25  
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24

<210> 26  
<211> 422  
<212> PRT  
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<223> Description of Artificial Sequence: mutated human  
MCH1

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<400> 26
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      1           5           10          15

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Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp  
..... 20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro  
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala  
50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly  
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala  
85 90 95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met  
100 105 110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser  
115 120 125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn  
130 135 140

Asn	Val	Pro	Asp	Ile	Phe	Ile	Ile	Asn	Leu	Ser	Val	Val	Asp	Leu	Leu
145					150					155					160

Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly  
165 170 175

12

Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp  
           180                     185                     190  
  
 Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile  
           195                     200                     205  
  
 Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg  
           210                     215                     220  
  
 Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser  
           225                     230                     235                     240  
  
 Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe  
           245                     250                     255  
  
 Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr  
           260                     265                     270  
  
 Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu  
           275                     280                     285  
  
 Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met  
           290                     295                     300  
  
 Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr  
           305                     310                     315                     320  
  
 Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val  
           325                     330                     335  
  
 Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser  
           340                     345                     350  
  
 Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu  
           355                     360                     365  
  
 Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys  
           370                     375                     380  
  
 Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln  
           385                     390                     395                     400  
  
 Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg  
           405                     410                     415  
  
 Thr Glu Ser Lys Gly Thr  
           420

MUSICO-225860

<210> 27  
<211> 422  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: mutated human  
MCH1

<400> 27

Met	Ser	Val	Gly	Ala	Ala	Lys	Lys	Gly	Val	Gly	Arg	Ala	Val	Gly	Leu
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Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp

20						25							30		
----	--	--	--	--	--	----	--	--	--	--	--	--	----	--	--

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro

35					40							45		
----	--	--	--	--	----	--	--	--	--	--	--	----	--	--

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala

50				55				60						
----	--	--	--	----	--	--	--	----	--	--	--	--	--	--

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly

65			70			75					80			
----	--	--	----	--	--	----	--	--	--	--	----	--	--	--

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala

85					90						95			
----	--	--	--	--	----	--	--	--	--	--	----	--	--	--

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met

100				105			110							
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser

115				120			125							
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn

130				135			140							
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu

145				150			155				160			
-----	--	--	--	-----	--	--	-----	--	--	--	-----	--	--	--

Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly

165					170			175						
-----	--	--	--	--	-----	--	--	-----	--	--	--	--	--	--

Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp

180				185			190							
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile  
 195 200 205  
 Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg  
 210 215 220  
 Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser  
 225 230 235 240  
 Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe  
 245 250 255  
 Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr  
 260 265 270  
 Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu  
 275 280 285  
 Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met  
 290 295 300  
 Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr  
 305 310 315 320  
 Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val  
 325 330 335  
 Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser  
 340 345 350  
 Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu  
 355 360 365  
 Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys  
 370 375 380  
 Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln  
 385 390 395 400  
 Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg  
 405 410 415  
 Thr Glu Ser Lys Gly Thr  
 420

<210> 28  
 <211> 353

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mutated human  
MCH1

<400> 28

Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly Pro Asn Ala Ser Asn  
1 5 10 15

Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala Gly Ser Pro Pro Arg  
20 25 30

Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly  
35 40 45

Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser Thr Val Ile Phe Ala  
50 55 60

Val Val Lys Lys Ser Lys Leu His Trp Cys Asn Asn Val Pro Asp Ile  
65 70 75 80

Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met  
85 90 95

Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly  
100 105 110

Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe  
115 120 125

Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile Asp Arg Tyr Leu Ala  
130 135 140

Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Val Ala  
145 150 155 160

Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr  
165 170 175

Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val  
180 185 190

Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe  
195 200 205

Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile

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210	215	220
Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met Thr Ser Ser Val Ala		
225	230	235
240		245
Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg		
245		250
		255
Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr		
260	265	270
Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr		
275	280	285
Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser		
290	295	300
Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys		
305	310	315
320		325
Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Ala		
325	330	335
Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly		
340	345	350
Thr		